

0307

#12



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/714,712A

DATE: 03/07/2002 P.S
TIME: 13:36:04

Input Set : A:\EP.txt

Output Set: N:\CRF3\03072002\I714712A.raw

3 <110> APPLICANT: Schmitz, et al.

5 <120> TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS SPECIFIC FOR DENDRITIC CELLS
COMPOSITIONS AND

6 METHODS OF USE THEREOF ANTIGENS RECOGNIZED THEREBY AND CELLS OBTAINED THEREBY

8 <130> FILE REFERENCE: 830003-2002.1

10 <140> CURRENT APPLICATION NUMBER: 09/714,712A

11 <141> CURRENT FILING DATE: 2000-11-15

13 <150> PRIOR APPLICATION NUMBER: 60/165,555

14 <151> PRIOR FILING DATE: 1999-11-15

16 <160> NUMBER OF SEQ ID NOS: 38

18 <170> SOFTWARE: PatentIn version 3.0

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 1312

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

25 <220> FEATURE:

26 <221> NAME/KEY: misc_feature

27 <222> LOCATION: (1)..(1312)

28 <223> OTHER INFORMATION: BDCA-2 cDNA sequence

31 <400> SEQUENCE: 1

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32 cagtgattct cgtgcctcag cctcctgagt agccgaaatt acagacgtgt gccaccatgc      60
34 ttggctaatt ttttgattt ttagtagaga tggggtttca ctatgttggc caggctagtc      120
36 ttgaactcct ggcctgaagc aatccgcca cctcagcctc ccaaagtgt gagattatag      180
38 gcacgagcca ctacacctgg ccacaaaatt ctttaaagaa gccaatccca tcctccctca      240
40 agagccaagg ggccacctca ccctcttggt acagcagatc ctgcctccac agtcaccctg      300
42 ctcccaagtg caacctctgt ctgacctgc atggtgtgct gtgccctcct gectcaggcc      360
44 gcgaagaagg atctaagggc ttggttgtt tgaaagaacc acaccccgaa agtaacatct      420
46 ttggagaaag tgatacaaga gttctgcac ccacctgata gaggaagtcc aaagggtgtg      480
48 gcgcacacaca atggtgcctg aagaagagcc tcaagaccga gagaaaggac tctggtggtt      540
50 ccagttgaag gtctggtcca tggcagtcgt atccatcttg ctctcagtg tctgtttcac      600
52 tgtgagttct gtggtgcctc acaattttat gtatagcaaa actgtcaaga ggctgtccaa      660
54 gttacgagag tatcaacagt atcatccaag cctgacctgc gtcattggaag gaaaggacat      720
56 agaagatttg agctgctgcc caaccccttg gacttcattt cagtctagtt gctactttat      780
58 ttctactggg atgcaatctt ggactaagag tcaaaagaac tgttctgtga tgggggctga      840
60 tctggtggtg atcaacacca gggaagaaca ggatttcac attcagaatc tgaaaagaaa      900
62 ttcttcttat tttctggggc tgtcagatcc agggggtcgg cgacattggc aatgggttga      960
64 ccagacacca tacaatgaaa atgtcacatt ctggcactca ggtgaaccca ataacctga      1020
66 tgagcgttgt gcgataataa atttccggtt ttcagaagaa tggggctgga atgacattca      1080
68 ctgtcatgta cctcagaagt caatttgcaa gatgaagaag atctacatat aaatgaaata      1140
70 ttctccctgg aaatgtgtt gggttggcat ccaccgttgt agaaagctaa attgattttt      1200
72 taatttatgt gtaagttttg tacaaggaat gccctaaaaa tgtttcagca ggctgtcacc      1260
74 tattacactt atgatataat ccaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa      1312

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77 <210> SEQ ID NO: 2

78 <211> LENGTH: 213

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Input Set : A:\EP.txt

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79 <212> TYPE: PRT
 80 <213> ORGANISM: Homo sapiens
 82 <220> FEATURE:
 83 <221> NAME/KEY: UNSURE
 84 <222> LOCATION: (1)..(213)
 85 <223> OTHER INFORMATION: amino acid sequence of one of the isoforms of BDCA-2 with all
 six
 87 exons expressed
 90 <400> SEQUENCE: 2
 92 Met Val Pro Glu Glu Glu Pro Gln Asp Arg Glu Lys Gly Leu Trp Trp
 93 1 5 10 15
 95 Phe Gln Leu Lys Val Trp Ser Met Ala Val Val Ser Ile Leu Leu Leu
 96 20 25 30
 98 Ser Val Cys Phe Thr Val Ser Ser Val Val Pro His Asn Phe Met Tyr
 99 35 40 45
 101 Ser Lys Thr Val Lys Arg Leu Ser Lys Leu Arg Glu Tyr Gln Gln Tyr
 102 50 55 60
 104 His Pro Ser Leu Thr Cys Val Met Glu Gly Lys Asp Ile Glu Asp Trp
 105 65 70 75 80
 107 Ser Cys Cys Pro Thr Pro Trp Thr Ser Phe Gln Ser Ser Cys Tyr Phe
 108 85 90 95
 110 Ile Ser Thr Gly Met Gln Ser Trp Thr Lys Ser Gln Lys Asn Cys Ser
 111 100 105 110
 113 Val Met Gly Ala Asp Leu Val Val Ile Asn Thr Arg Glu Glu Gln Asp
 114 115 120 125
 116 Phe Ile Ile Gln Asn Leu Lys Arg Asn Ser Ser Tyr Phe Leu Gly Leu
 117 130 135 140
 119 Ser Asp Pro Gly Gly Arg Arg His Trp Gln Trp Val Asp Gln Thr Pro
 120 145 150 155 160
 122 Tyr Asn Glu Asn Val Thr Phe Trp His Ser Gly Glu Pro Asn Asn Leu
 123 165 170 175
 125 Asp Glu Arg Cys Ala Ile Ile Asn Phe Arg Ser Ser Glu Glu Trp Gly
 126 180 185 190
 128 Trp Asn Asp Ile His Cys His Val Pro Gln Lys Ser Ile Cys Lys Met
 129 195 200 205
 131 Lys Lys Ile Tyr Ile
 132 210
 134 <210> SEQ ID NO: 3
 135 <211> LENGTH: 1227
 136 <212> TYPE: DNA
 137 <213> ORGANISM: Mus musculus
 139 <220> FEATURE:
 140 <221> NAME/KEY: CDS
 141 <222> LOCATION: (146)..(775)
 142 <223> OTHER INFORMATION: coding sequence of mouse Dectin-2
 145 <300> PUBLICATION INFORMATION:
 146 <308> DATABASE ACCESSION NO: AF240357
 147 <309> DATABASE ENTRY DATE: 2000-05-02
 148 <313> RELEVANT RESIDUES: (1)..(1227)
 150 <400> SEQUENCE: 3

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151 cattggcccg ctctgtggca tttaactcaa gtgtgtgtgg aagttgattc tgaactctgg      60
153 cctctttgac agaagccagg tccctgagtc gtattttgga gacagatgca agaaaccct      120
155 gaccttctga acatacacct caaca atg gtg cag gaa aga caa tcc caa ggg      172
156                               Met Val Gln Glu Arg Gln Ser Gln Gly
157                               1                               5
159 aag gga gtc tgc tgg acc ctg aga ctc tgg tca gct gct gtg att tcc      220
160 Lys Gly Val Cys Trp Thr Leu Arg Leu Trp Ser Ala Ala Val Ile Ser
161 10                               15                               20                               25
163 atg tta ctc ttg agt acc tgt ttc att gcg agc tgt gtg gtg act tac      268
164 Met Leu Leu Leu Ser Thr Cys Phe Ile Ala Ser Cys Val Val Thr Tyr
165                               30                               35                               40
167 caa ttt att atg gac cag ccc agt aga aga cta tat gaa ctt cac aca      316
168 Gln Phe Ile Met Asp Gln Pro Ser Arg Arg Leu Tyr Glu Leu His Thr
169                               45                               50                               55
171 tac cat tcc agt ctc acc tgc ttc agt gaa ggg act atg gtg tca gaa      364
172 Tyr His Ser Ser Leu Thr Cys Phe Ser Glu Gly Thr Met Val Ser Glu
173                               60                               65                               70
175 aaa atg tgg gga tgc tgc cca aat cac tgg aag tca ttt ggc tcc agc      412
176 Lys Met Trp Gly Cys Cys Pro Asn His Trp Lys Ser Phe Gly Ser Ser
177                               75                               80                               85
179 tgc tac ctc att tct acc aag gag aac ttc tgg agc acc agt gag cag      460
180 Cys Tyr Leu Ile Ser Thr Lys Glu Asn Phe Trp Ser Thr Ser Glu Gln
181 90                               95                               100                               105
183 aac tgt gtt cag atg ggg gct cat ctg gtg gtg atc aat act gaa gcg      508
184 Asn Cys Val Gln Met Gly Ala His Leu Val Val Ile Asn Thr Glu Ala
185                               110                               115                               120
187 gag cag aat ttc atc acc cag cag ctg aat gag tca ctt tct tac ttc      556
188 Glu Gln Asn Phe Ile Thr Gln Gln Leu Asn Glu Ser Leu Ser Tyr Phe
189                               125                               130                               135
191 ctg ggt ctt tcg gat cca caa ggt aat ggc aaa tgg caa tgg atc gat      604
192 Leu Gly Leu Ser Asp Pro Gln Gly Asn Gly Lys Trp Gln Trp Ile Asp
193                               140                               145                               150
195 gat act cct ttc agt caa aat gtc agg ttc tgg cac ccc cat gaa ccc      652
196 Asp Thr Pro Phe Ser Gln Asn Val Arg Phe Trp His Pro His Glu Pro
197                               155                               160                               165
199 aat ctt cca gaa gag cgg tgt gtt tca ata gtt tac tgg aat cct tcg      700
200 Asn Leu Pro Glu Glu Arg Cys Val Ser Ile Val Tyr Trp Asn Pro Ser
201 170                               175                               180                               185
203 aaa tgg ggc tgg aat gat gtt ttc tgt gat agt aaa cac aat tca ata      748
204 Lys Trp Gly Trp Asn Asp Val Phe Cys Asp Ser Lys His Asn Ser Ile
205                               190                               195                               200
207 tgt gaa atg aag aag att tac cta tga gtgcctgtta ttcattaata      795
208 Cys Glu Met Lys Lys Ile Tyr Leu
209                               205
211 tcttttaaagt tcagacctac caagaagcca taacttcttg gcctgtacat ctgacagagg      855
213 ccgttctttt cctagccact attctttact caaacagaat gagccctttc tccttctgat      915
215 ggtagagatt ttgtcaactt gacacaaact agagtcacct ggggagtagg atcttcagct      975
217 aaggaattgc ctctgtcagc ttgaccagtc agcatgtctg ggggcatttt cttgattaat      1035
219 gattgtttgta agaggggtcca ggtggttaagc aaaggtgtta aacccatgaa gagcaagcca      1095

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221 gggagcatca tccatccatc tctgccctca ggtttctgcc ccagggtctt gccctggttt 1155
223 ctttctatga actgctgtta cttgaaagta taagatgaat aaacaatttc atccaaaaaa 1215
225 aaaaaaaaaa aa 1227
228 <210> SEQ ID NO: 4
229 <211> LENGTH: 209
230 <212> TYPE: PRT
231 <213> ORGANISM: Mus musculus
233 <400> SEQUENCE: 4
235 Met Val Gln Glu Arg Gln Ser Gln Gly Lys Gly Val Cys Trp Thr Leu
236 1 5 10 15
239 Arg Leu Trp Ser Ala Ala Val Ile Ser Met Leu Leu Leu Ser Thr Cys
240 20 25 30
243 Phe Ile Ala Ser Cys Val Val Thr Tyr Gln Phe Ile Met Asp Gln Pro
244 35 40 45
247 Ser Arg Arg Leu Tyr Glu Leu His Thr Tyr His Ser Ser Leu Thr Cys
248 50 55 60
251 Phe Ser Glu Gly Thr Met Val Ser Glu Lys Met Trp Gly Cys Cys Pro
252 65 70 75 80
255 Asn His Trp Lys Ser Phe Gly Ser Ser Cys Tyr Leu Ile Ser Thr Lys
256 85 90 95
259 Glu Asn Phe Trp Ser Thr Ser Glu Gln Asn Cys Val Gln Met Gly Ala
260 100 105 110
263 His Leu Val Val Ile Asn Thr Glu Ala Glu Gln Asn Phe Ile Thr Gln
264 115 120 125
267 Gln Leu Asn Glu Ser Leu Ser Tyr Phe Leu Gly Leu Ser Asp Pro Gln
268 130 135 140
271 Gly Asn Gly Lys Trp Gln Trp Ile Asp Asp Thr Pro Phe Ser Gln Asn
272 145 150 155 160
275 Val Arg Phe Trp His Pro His Glu Pro Asn Leu Pro Glu Glu Arg Cys
276 165 170 175
279 Val Ser Ile Val Tyr Trp Asn Pro Ser Lys Trp Gly Trp Asn Asp Val
280 180 185 190
283 Phe Cys Asp Ser Lys His Asn Ser Ile Cys Glu Met Lys Lys Ile Tyr
284 195 200 205
287 Leu
291 <210> SEQ ID NO: 5
292 <211> LENGTH: 237
293 <212> TYPE: PRT
294 <213> ORGANISM: Homo sapiens
296 <220> FEATURE:
297 <221> NAME/KEY: UNSURE
298 <222> LOCATION: (1)..(237)
299 <223> OTHER INFORMATION: amino acid sequence of human DCIR
302 <300> PUBLICATION INFORMATION:
303 <308> DATABASE ACCESSION NO: AJ133532
304 <309> DATABASE ENTRY DATE: 1999-09-01
305 <313> RELEVANT RESIDUES: (1)..(237)
307 <400> SEQUENCE: 5
309 Met Thr Ser Glu Ile Thr Tyr Ala Glu Val Arg Phe Lys Asn Glu Phe

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```

310 1          5          10          15
312 Lys Ser Ser Gly Ile Asn Thr Ala Ser Ser Ala Ala Ser Lys Glu Arg
313          20          25          30
315 Thr Ala Pro His Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala
316          35          40          45
318 Ser Leu Leu Ile Phe Phe Leu Leu Ala Ile Ser Phe Phe Ile Ala
319          50          55          60
321 Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr
322 65          70          75          80
324 Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met
325          85          90          95
327 Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser
328          100          105          110
330 Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln
331          115          120          125
333 Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile
334          130          135          140
336 Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu
337 145          150          155          160
339 Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp
340          165          170          175
342 Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His
343          180          185          190
345 Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe
346          195          200          205
348 Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly
349          210          215          220
351 Pro Gln Arg Ser Val Cys Glu Met Met Lys Ile His Leu
352 225          230          235
354 <210> SEQ ID NO: 6
355 <211> LENGTH: 5
356 <212> TYPE: PRT
357 <213> ORGANISM: Artificial Sequence
359 <220> FEATURE:
360 <223> OTHER INFORMATION: basic unit of a linking peptide
362 <400> SEQUENCE: 6
364 Gly Gly Gly Gly Ser
365 1          5
367 <210> SEQ ID NO: 7
368 <211> LENGTH: 24
369 <212> TYPE: DNA
370 <213> ORGANISM: Artificial Sequence
372 <220> FEATURE:
373 <223> OTHER INFORMATION: primer
375 <400> SEQUENCE: 7
376 ttgaaagaac cacaccccgga aagt
379 <210> SEQ ID NO: 8
380 <211> LENGTH: 24
381 <212> TYPE: DNA

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24

→ Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/714,712A

DATE: 03/07/2002

TIME: 13:36:05

Input Set : A:\EP.txt

Output Set: N:\CRF3\03072002\I714712A.raw

L:737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37